UniProtKB/Swiss-Prot entry O84883

Entry information

Entry name	**Y875_CHLTR**
Primary accession number	**O84883**
Secondary accession numbers	None
Integrated into Swiss-Prot on	April 27, 2001
Sequence was last modified on	November 1, 1998 (Sequence version 1)
Annotations were last modified on	October 31, 2006 (Entry version 28)

Name and origin of the protein

Protein name	**Protein CT_875**
Synonyms	None
Gene name	OrderedLocusNames: CT_875
From	Chlamydia trachomatis [TaxID: 813] [HAMAP proteome]
Taxonomy	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=D/UW-3/Cx;
DOI=10.1126/science.282.5389.754; PubMed=9784136
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).

Comments

- **SIMILARITY:** To C.muridarum TC_0268.

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Cross-references

Sequence databases	
EMBL	AE001273; AAC68473.1; -; Genomic_DNA.
PIR	C71460; C71460.
2D gel databases	
PHCi-2DPAGE	O84883; -.
Genome annotation databases	
GenomeReviews	AE001273_GR; CT_875.
KEGG	ctr:CT875; -.
Other	
Implict links to	CMR; ProDom; HOGENOM; BLOCKS; ProtoNet; ModBase; UniRef.

Keywords

Complete proteome.

Features

Key	From	To	Length	Description	FTId
CHAIN	1	591	591	Protein CT_875.	PRO_0000218349

Sequence Information

Length: **591 AA** [This is the length of the unprocessed precursor]
Molecular weight: **66076 Da** [This is the MW of the unprocessed precursor]
CRC64: **B21C0127FDBB2EC8** [This is a checksum on the sequence]

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        10         20         30         40         50         60
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           70         80         90        100        110        120
MSIRGVGGNG NSRIPSHNGD GSNRRSQNTK GNNKVEDRVC SLYSSRSNEN RESPYAVVDV
          130        140        150        160        170        180
SSMIESTPTS GETTRASRGV FSRFQRGLVR VADKVRRAVQ CAWSSVSTRR SSATRAAESG
          190        200        210        220        230        240
SSSRTARGAS SGYREYSPSA ARGLRLMFTD FWRTRVLRQT SPMAGVFGNL DVNEARLMAA
          250        260        270        280        290        300
YTSECADHLE ANKLAGPDGV AAAREIAKRW EQRVRDLQDK GAARKLLNDP LGRRTPNYQS
          310        320        330        340        350        360
KNPGEYTVGN SMFYDGPQVA NLQNVDTGFW LDMSNLSDVV LSREIQTGLR ARATLEESMP
          370        380        390        400        410        420
MLENLEERFR RLQETCDAAR TEIEESGWTR ESASRMEGDE AQGPSRAQQA FQSFVNECNS
          430        440        450        460        470        480
IEFSFGSFGE HVRVLCARVS RGLAAAGEAI RRCFSCCKGS THRYAPRDDL SPEGASLAET
          490        500        510        520        530        540
LARFADDMGI ERGADGTYDI PLVDDWRRGV PSIEGEGSDS IYEINMPIYE VMDMDLETRR
          550        560        570        580        590
SFAVQQGHYQ DPRASDYDLP RASDYDLPRS PYPTPFLPPR YQLQNMDVEA GFREAVYASF
VAGMYNYVVT QPQERIPNSQ QVEGILRDML TNGSQTFRDL MRRWNREVDR E
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